



SEQUENCE LISTING

RECEIVED
JUL 3 2002
TECH CENTER 1600/2900

<110> ANDERSON, Dirk, M.
GALIBERT, Laurent, J.

<120> METHOD OF INHIBITING OSTEOCLAST ACTIVITY

<130> 2874-B

<140> 09/705,985

<141> 2000-11-03

<150> PCT/US99/10588

<151> 1999-05-13

<150> 60/085,487

<151> 1998-05-14

<150> 60/110,836

<151> 1998-12-03

<150> 08/996,139

<151> 1997-12-22

<150> 60/064,671

<151> 1997-10-14

<150> 60/077,181

<151> 1997-03-07

<150> 60/059,978

<151> 1996-12-23

<160> 8

<170> PatentIn version 3.1

<210> 1

<211> 3136

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (39)..(1886)

<223>

<400> 1

ccgctgagggc cgcggcgccc gccagcctgt cccgcgcc atg gcc ccg cgc gcc cgg 56
Met Ala Pro Arg Ala Arg
1 5

cgg cgc cgc ccg ctg ttc gcg ctg ctg ctg ctc tgc gcg ctg ctc gcc 104
Arg Arg Arg Pro Leu Phe Ala Leu Leu Leu Leu Cys Ala Leu Leu Ala
10 15 20

cgg ctg cag gtg gct ttg cag atc gct cct cca tgt acc agt gag aag 152
Arg Leu Gln Val Ala Leu Gln Ile Ala Pro Pro Cys Thr Ser Glu Lys
25 30 35

cat tat gag cat ctg gga cgg tgc tgt aac aaa tgt gaa cca gga aag	200
His Tyr Glu His Leu Gly Arg Cys Cys Asn Lys Cys Glu Pro Gly Lys	
40 45 50	
tac atg tct tct aaa tgc act act acc tct gac agt gta tgt ctg ccc	248
Tyr Met Ser Ser Lys Cys Thr Thr Thr Ser Asp Ser Val Cys Leu Pro	
55 60 65 70	
tgt ggc ccg gat gaa tac ttg gat agc tgg aat gaa gaa gat aaa tgc	296
Cys Gly Pro Asp Glu Tyr Leu Asp Ser Trp Asn Glu Glu Asp Lys Cys	
75 80 85	
ttg ctg cat aaa gtt tgt gat aca ggc aag gcc ctg gtg gcc gtg gtc	344
Leu Leu His Lys Val Cys Asp Thr Gly Lys Ala Leu Val Ala Val Val	
90 95 100	
gcc ggc aac agc acg acc ccc cgg cgc tgc gcg tgc acg gct ggg tac	392
Ala Gly Asn Ser Thr Thr Pro Arg Arg Cys Ala Cys Thr Ala Gly Tyr	
105 110 115	
cac tgg agc cag gac tgc gag tgc tgc cgc cgc aac acc gag tgc gcg	440
His Trp Ser Gln Asp Cys Glu Cys Cys Arg Arg Asn Thr Glu Cys Ala	
120 125 130	
ccg ggc ctg ggc gcc cag cac ccg ttg cag ctc aac aag gac aca gtg	488
Pro Gly Leu Gly Ala Gln His Pro Leu Gln Leu Asn Lys Asp Thr Val	
135 140 145 150	
tgc aaa cct tgc ctt gca ggc tac ttc tct gat gcc ttt tcc tcc acg	536
Cys Lys Pro Cys Leu Ala Gly Tyr Phe Ser Asp Ala Phe Ser Ser Thr	
155 160 165	
gac aaa tgc aga ccc tgg acc aac tgt acc ttc ctt gga aag aga gta	584
Asp Lys Cys Arg Pro Trp Thr Asn Cys Thr Phe Leu Gly Lys Arg Val	
170 175 180	
gaa cat cat ggg aca gag aaa tcc gat gcg gtt tgc agt tct tct ctg	632
Glu His His Gly Thr Glu Lys Ser Asp Ala Val Cys Ser Ser Ser Leu	
185 190 195	
cca gct aga aaa cca cca aat gaa ccc cat gtt tac ttg ccc ggt tta	680
Pro Ala Arg Lys Pro Pro Asn Glu Pro His Val Tyr Leu Pro Gly Leu	
200 205 210	
ata att ctg ctt ctc ttc gcg tct gtg gcc ctg gtg gct gcc atc atc	728
Ile Ile Leu Leu Leu Phe Ala Ser Val Ala Leu Val Ala Ala Ile Ile	
215 220 225 230	
ttt ggc gtt tgc tat agg aaa aaa ggg aaa gca ctc aca gct aat ttg	776
Phe Gly Val Cys Tyr Arg Lys Lys Gly Lys Ala Leu Thr Ala Asn Leu	
235 240 245	
tgg cac tgg atc aat gag gct tgt ggc cgc cta agt gga gat aag gag	824
Trp His Trp Ile Asn Glu Ala Cys Gly Arg Leu Ser Gly Asp Lys Glu	
250 255 260	
tcc tca ggt gac agt tgt gtc agt aca cac acg gca aac ttt ggt cag	872
Ser Ser Gly Asp Ser Cys Val Ser Thr His Thr Ala Asn Phe Gly Gln	
265 270 275	
cag gga gca tgt gaa ggt gtc tta ctg ctg act ctg gag gag aag aca	920

Gln	Gly	Ala	Cys	Glu	Gly	Val	Leu	Leu	Leu	Thr	Leu	Glu	Glu	Lys	Thr	
280						285					290					
ttt	cca	gaa	gat	atg	tgc	tac	cca	gat	caa	ggg	ggg	gtc	tgt	cag	ggc	968
Phe	Pro	Glu	Asp	Met	Cys	Tyr	Pro	Asp	Gln	Gly	Gly	Val	Cys	Gln	Gly	
295					300					305					310	
acg	tgt	gta	gga	ggg	ggg	ccc	tac	gca	caa	ggc	gaa	gat	gcc	agg	atg	1016
Thr	Cys	Val	Gly	Gly	Gly	Pro	Tyr	Ala	Gln	Gly	Glu	Asp	Ala	Arg	Met	
				315					320					325		
ctc	tca	ttg	gtc	agc	aag	acc	gag	ata	gag	gaa	gac	agc	ttc	aga	cag	1064
Leu	Ser	Leu	Val	Ser	Lys	Thr	Glu	Ile	Glu	Glu	Asp	Ser	Phe	Arg	Gln	
			330					335						340		
atg	ccc	aca	gaa	gat	gaa	tac	atg	gac	agg	ccc	tcc	cag	ccc	aca	gac	1112
Met	Pro	Thr	Glu	Asp	Glu	Tyr	Met	Asp	Arg	Pro	Ser	Gln	Pro	Thr	Asp	
		345					350					355				
cag	tta	ctg	ttc	ctc	act	gag	cct	gga	agc	aaa	tcc	aca	cct	cct	ttc	1160
Gln	Leu	Leu	Phe	Leu	Thr	Glu	Pro	Gly	Ser	Lys	Ser	Thr	Pro	Pro	Phe	
	360					365					370					
tct	gaa	ccc	ctg	gag	gtg	ggg	gag	aat	gac	agt	tta	agc	cag	tgc	ttc	1208
Ser	Glu	Pro	Leu	Glu	Val	Gly	Glu	Asn	Asp	Ser	Leu	Ser	Gln	Cys	Phe	
375					380					385					390	
acg	ggg	aca	cag	agc	aca	gtg	ggg	tca	gaa	agc	tgc	aac	tgc	act	gag	1256
Thr	Gly	Thr	Gln	Ser	Thr	Val	Gly	Ser	Glu	Ser	Cys	Asn	Cys	Thr	Glu	
				395					400					405		
ccc	ctg	tgc	agg	act	gat	tgg	act	ccc	atg	tcc	tct	gaa	aac	tac	ttg	1304
Pro	Leu	Cys	Arg	Thr	Asp	Trp	Thr	Pro	Met	Ser	Ser	Glu	Asn	Tyr	Leu	
			410					415						420		
caa	aaa	gag	gtg	gac	agt	ggc	cat	tgc	ccg	cac	tgg	gca	gcc	agc	ccc	1352
Gln	Lys	Glu	Val	Asp	Ser	Gly	His	Cys	Pro	His	Trp	Ala	Ala	Ser	Pro	
		425					430					435				
agc	ccc	aac	tgg	gca	gat	gtc	tgc	aca	ggc	tgc	cgg	aac	cct	cct	ggg	1400
Ser	Pro	Asn	Trp	Ala	Asp	Val	Cys	Thr	Gly	Cys	Arg	Asn	Pro	Pro	Gly	
	440					445					450					
gag	gac	tgt	gaa	ccc	ctc	gtg	ggg	tcc	cca	aaa	cgt	gga	ccc	ttg	ccc	1448
Glu	Asp	Cys	Glu	Pro	Leu	Val	Gly	Ser	Pro	Lys	Arg	Gly	Pro	Leu	Pro	
455					460					465					470	
cag	tgc	gcc	tat	ggc	atg	ggc	ctt	ccc	cct	gaa	gaa	gaa	gcc	agc	agg	1496
Gln	Cys	Ala	Tyr	Gly	Met	Gly	Leu	Pro	Pro	Glu	Glu	Glu	Ala	Ser	Arg	
				475					480					485		
acg	gag	gcc	aga	gac	cag	ccc	gag	gat	ggg	gct	gat	ggg	agg	ctc	cca	1544
Thr	Glu	Ala	Arg	Asp	Gln	Pro	Glu	Asp	Gly	Ala	Asp	Gly	Arg	Leu	Pro	
			490					495					500			
agc	tca	gcg	agg	gca	ggg	gcc	ggg	tct	gga	agc	tcc	cct	ggg	ggc	cag	1592
Ser	Ser	Ala	Arg	Ala	Gly	Ala	Gly	Ser	Gly	Ser	Ser	Pro	Gly	Gly	Gln	
		505					510					515				
tcc	cct	gca	tct	gga	aat	gtg	act	gga	aac	agt	aac	tcc	acg	ttc	atc	1640
Ser	Pro	Ala	Ser	Gly	Asn	Val	Thr	Gly	Asn	Ser	Asn	Ser	Thr	Phe	Ile	

520	525	530	
tcc agc ggg cag gtg atg aac ttc aag ggc gac	atc atc gtg gtc tac	1688	
Ser Ser Gly Gln Val Met Asn Phe Lys Gly Asp	Ile Ile Val Val Tyr		
535	540 545 550		
gtc agc cag acc tcg cag gag ggc gcg gcg gct gcg gag ccc atg	1736		
Val Ser Gln Thr Ser Gln Glu Gly Ala Ala Ala Ala Ala Glu Pro Met			
555	560 565		
ggc cgc ccg gtg cag gag gag acc ctg gcg cgc cga gac tcc ttc gcg	1784		
Gly Arg Pro Val Gln Glu Glu Thr Leu Ala Arg Arg Asp Ser Phe Ala			
570	575 580		
ggg aac ggc ccg cgc ttc ccg gac ccg tgc ggc ggc ccc gag ggg ctg	1832		
Gly Asn Gly Pro Arg Phe Pro Asp Pro Cys Gly Gly Pro Glu Gly Leu			
585	590 595		
cgg gag ccg gag aag gcc tcg agg ccg gtg cag gag caa ggc ggg gcc	1880		
Arg Glu Pro Glu Lys Ala Ser Arg Pro Val Gln Glu Gln Gly Gly Ala			
600	605 610		
aag gct tgagcgcccc ccatggctgg gagcccgaag ctccggagcca gggctcgca	1936		
Lys Ala			
615			
gggcagcacc gcagcctctg cccagcccc ggccacccag ggatcgatcg gtacagtcga	1996		
ggaagaccac ccggcattct ctgccactt tgccttcag gaaatgggct tttcaggaag	2056		
tgaattgatg aggactgtcc ccatgcccac ggatgctcag cagcccgcg cactggggca	2116		
gatgtctccc ctgccactcc tcaaactcgc agcagtaatt tgtggcacta tgacagctat	2176		
ttttatgact atcctgttct gtgggggggg ggtctatggt tccccccat atttgatttc	2236		
cttttcataa cttttcttga tatctttcct ccctcttttt taatgtaaag gttttctcaa	2296		
aaattctcct aaagggtgagg gtctctttct tttctctttt cttttttttt ttcttttttt	2356		
ggcaacctgg ctctggccca ggctagagtg cagtgggtgcg attatagccc ggtgcagcct	2416		
ctaactcctg ggctcaagca atccaagtga tcctcccacc tcaaccttcg gagtagctgg	2476		
gatcacagct gcaggccacg ccagcttcc tccccccgac tccccccccc cagagacacg	2536		
gtcccaccat gttaccacagc ctggtctcaa actccccagc taaagcagtc ctccagcctc	2596		
ggcctcccaa agtactggga ttacaggcgt gagccccac gctggcctgc tttacgtatt	2656		
ttcttttgtg cccctgctca cagtgtttta gagatggctt tcccagtggtg tgttcattgt	2716		
aaacactttt gggaaagggc taaacatgtg aggcctggag atagttgcta agttgctagg	2776		
aacatgtggt gggactttca tattctgaaa aatgttctat attctcattt ttctaaaaga	2836		
aagaaaaaag gaaacccgat ttatttctcc tgaatctttt taagtttggtg tcgttcctta	2896		
agcagaacta agctcagtat gtgaccttac ccgctaggtg gttaatttat ccatgctggc	2956		
agaggcactc aggtacttgg taagcaaatt tctaaaactc caagttgctg cagcttggca	3016		

ttctttcttat tctagaggtc tctctggaaa agatggagaa aatgaacagg acatggggct 3076

cctggaaaga aagggcccgg gaagttcaag gaagaataaa gttgaaattt taaaaaaaaa 3136

<210> 2

<211> 616

<212> PRT

<213> Homo sapiens

<400> 2

Met Ala Pro Arg Ala Arg Arg Arg Arg Pro Leu Phe Ala Leu Leu Leu
1 5 10 15

Leu Cys Ala Leu Leu Ala Arg Leu Gln Val Ala Leu Gln Ile Ala Pro
20 25 30

Pro Cys Thr Ser Glu Lys His Tyr Glu His Leu Gly Arg Cys Cys Asn
35 40 45

Lys Cys Glu Pro Gly Lys Tyr Met Ser Ser Lys Cys Thr Thr Thr Ser
50 55 60

Asp Ser Val Cys Leu Pro Cys Gly Pro Asp Glu Tyr Leu Asp Ser Trp
65 70 75 80

Asn Glu Glu Asp Lys Cys Leu Leu His Lys Val Cys Asp Thr Gly Lys
85 90 95

Ala Leu Val Ala Val Val Ala Gly Asn Ser Thr Thr Pro Arg Arg Cys
100 105 110

Ala Cys Thr Ala Gly Tyr His Trp Ser Gln Asp Cys Glu Cys Cys Arg
115 120 125

Arg Asn Thr Glu Cys Ala Pro Gly Leu Gly Ala Gln His Pro Leu Gln
130 135 140

Leu Asn Lys Asp Thr Val Cys Lys Pro Cys Leu Ala Gly Tyr Phe Ser
145 150 155 160

Asp Ala Phe Ser Ser Thr Asp Lys Cys Arg Pro Trp Thr Asn Cys Thr
165 170 175

Phe Leu Gly Lys Arg Val Glu His His Gly Thr Glu Lys Ser Asp Ala
180 185 190

Val Cys Ser Ser Ser Leu Pro Ala Arg Lys Pro Pro Asn Glu Pro His
 195 200 205

Val Tyr Leu Pro Gly Leu Ile Ile Leu Leu Leu Phe Ala Ser Val Ala
 210 215 220

Leu Val Ala Ala Ile Ile Phe Gly Val Cys Tyr Arg Lys Lys Gly Lys
 225 230 235 240

Ala Leu Thr Ala Asn Leu Trp His Trp Ile Asn Glu Ala Cys Gly Arg
 245 250 255

Leu Ser Gly Asp Lys Glu Ser Ser Gly Asp Ser Cys Val Ser Thr His
 260 265 270

Thr Ala Asn Phe Gly Gln Gln Gly Ala Cys Glu Gly Val Leu Leu Leu
 275 280 285

Thr Leu Glu Glu Lys Thr Phe Pro Glu Asp Met Cys Tyr Pro Asp Gln
 290 295 300

Gly Gly Val Cys Gln Gly Thr Cys Val Gly Gly Gly Pro Tyr Ala Gln
 305 310 315 320

Gly Glu Asp Ala Arg Met Leu Ser Leu Val Ser Lys Thr Glu Ile Glu
 325 330 335

Glu Asp Ser Phe Arg Gln Met Pro Thr Glu Asp Glu Tyr Met Asp Arg
 340 345 350

Pro Ser Gln Pro Thr Asp Gln Leu Leu Phe Leu Thr Glu Pro Gly Ser
 355 360 365

Lys Ser Thr Pro Pro Phe Ser Glu Pro Leu Glu Val Gly Glu Asn Asp
 370 375 380

Ser Leu Ser Gln Cys Phe Thr Gly Thr Gln Ser Thr Val Gly Ser Glu
 385 390 395 400

Ser Cys Asn Cys Thr Glu Pro Leu Cys Arg Thr Asp Trp Thr Pro Met
 405 410 415

Ser Ser Glu Asn Tyr Leu Gln Lys Glu Val Asp Ser Gly His Cys Pro
 420 425 430

His Trp Ala Ala Ser Pro Ser Pro Asn Trp Ala Asp Val Cys Thr Gly

435

440

445

Cys Arg Asn Pro Pro Gly Glu Asp Cys Glu Pro Leu Val Gly Ser Pro
 450 455 460

Lys Arg Gly Pro Leu Pro Gln Cys Ala Tyr Gly Met Gly Leu Pro Pro
 465 470 475 480

Glu Glu Glu Ala Ser Arg Thr Glu Ala Arg Asp Gln Pro Glu Asp Gly
 485 490 495

Ala Asp Gly Arg Leu Pro Ser Ser Ala Arg Ala Gly Ala Gly Ser Gly
 500 505 510

Ser Ser Pro Gly Gly Gln Ser Pro Ala Ser Gly Asn Val Thr Gly Asn
 515 520 525

Ser Asn Ser Thr Phe Ile Ser Ser Gly Gln Val Met Asn Phe Lys Gly
 530 535 540

Asp Ile Ile Val Val Tyr Val Ser Gln Thr Ser Gln Glu Gly Ala Ala
 545 550 555 560

Ala Ala Ala Glu Pro Met Gly Arg Pro Val Gln Glu Glu Thr Leu Ala
 565 570 575

Arg Arg Asp Ser Phe Ala Gly Asn Gly Pro Arg Phe Pro Asp Pro Cys
 580 585 590

Gly Gly Pro Glu Gly Leu Arg Glu Pro Glu Lys Ala Ser Arg Pro Val
 595 600 605

Gln Glu Gln Gly Gly Ala Lys Ala
 610 615

<210> 3
 <211> 232
 <212> PRT
 <213> Homo sapiens

<220>
 <221> PEPTIDE
 <222> (1) .. (232)
 <223>

<400> 3

Glu Pro Arg Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

1	5	10	15
Pro Glu Ala	Glu Gly Ala	Pro Ser Val	Phe Leu Phe Pro Pro Lys Pro
	20	25	30
Lys Asp Thr	Leu Met Ile	Ser Arg Thr	Pro Glu Val Thr Cys Val Val
	35	40	45
Val Asp Val	Ser His Glu	Asp Pro Glu	Val Lys Phe Asn Trp Tyr Val
	50	55	60
Asp Gly Val	Glu Val His	Asn Ala Lys	Thr Lys Pro Arg Glu Glu Gln
65	70		75 80
Tyr Asn Ser	Thr Tyr Arg	Val Val Ser	Val Leu Thr Val Leu His Gln
	85	90	95
Asp Trp Leu	Asn Gly Lys	Asp Tyr Lys	Cys Lys Val Ser Asn Lys Ala
	100	105	110
Leu Pro Ala	Pro Met Gln	Lys Thr Ile	Ser Lys Ala Lys Gly Gln Pro
	115	120	125
Arg Glu Pro	Gln Val Tyr	Thr Leu Pro	Pro Ser Arg Asp Glu Leu Thr
	130	135	140
Lys Asn Gln	Val Ser Leu	Thr Cys Leu	Val Lys Gly Phe Tyr Pro Arg
145	150		155 160
His Ile Ala	Val Glu Trp	Glu Ser Asn	Gly Gln Pro Glu Asn Asn Tyr
	165	170	175
Lys Thr Thr	Pro Pro Val	Leu Asp Ser	Asp Gly Ser Phe Phe Leu Tyr
	180	185	190
Ser Lys Leu	Thr Val Asp	Lys Ser Arg	Trp Gln Gln Gly Asn Val Phe
	195	200	205
Ser Cys Ser	Val Met His	Glu Ala Leu	His Asn His Tyr Thr Gln Lys
	210	215	220
Ser Leu Ser	Leu Ser Pro	Gly Lys	
225		230	

<210> 4
 <211> 1878

<212> DNA
<213> Murine

<220>
<221> CDS
<222> (1)..(1875)
<223>

<400> 4

atg gcc ccg cgc gcc cgg cgg cgc cgc cag ctg ccc gcg ccg ctg ctg	48
Met Ala Pro Arg Ala Arg Arg Arg Arg Gln Leu Pro Ala Pro Leu Leu	
1 5 10 15	
gcg ctc tgc gtg ctg ctc gtt cca ctg cag gtg act ctc cag gtc act	96
Ala Leu Cys Val Leu Leu Val Pro Leu Gln Val Thr Leu Gln Val Thr	
20 25 30	
cct cca tgc acc cag gag agg cat tat gag cat ctc gga cgg tgt tgc	144
Pro Pro Cys Thr Gln Glu Arg His Tyr Glu His Leu Gly Arg Cys Cys	
35 40 45	
agc aga tgc gaa cca gga aag tac ctg tcc tct aag tgc act cct acc	192
Ser Arg Cys Glu Pro Gly Lys Tyr Leu Ser Ser Lys Cys Thr Pro Thr	
50 55 60	
tcc gac agt gtg tgt ctg ccc tgt ggc ccc gat gag tac ttg gac acc	240
Ser Asp Ser Val Cys Leu Pro Cys Gly Pro Asp Glu Tyr Leu Asp Thr	
65 70 75 80	
tgg aat gaa gaa gat aaa tgc ttg ctg cat aaa gtc tgt gat gca ggc	288
Trp Asn Glu Glu Asp Lys Cys Leu Leu His Lys Val Cys Asp Ala Gly	
85 90 95	
aag gcc ctg gtg gcg gtg gat cct ggc aac cac acg gcc ccg cgt cgc	336
Lys Ala Leu Val Ala Val Asp Pro Gly Asn His Thr Ala Pro Arg Arg	
100 105 110	
tgt gct tgc acg gct ggc tac cac tgg aac tca gac tgc gag tgc tgc	384
Cys Ala Cys Thr Ala Gly Tyr His Trp Asn Ser Asp Cys Glu Cys Cys	
115 120 125	
cgc agg aac acg gag tgt gca cct ggc ttc gga gct cag cat ccc ttg	432
Arg Arg Asn Thr Glu Cys Ala Pro Gly Phe Gly Ala Gln His Pro Leu	
130 135 140	
cag ctc aac aag gat acg gtg tgc aca ccc tgc ctc ctg ggc ttc ttc	480
Gln Leu Asn Lys Asp Thr Val Cys Thr Pro Cys Leu Leu Gly Phe Phe	
145 150 155 160	
tca gat gtc ttt tcg tcc aca gac aaa tgc aaa cct tgg acc aac tgc	528
Ser Asp Val Phe Ser Ser Thr Asp Lys Cys Lys Pro Trp Thr Asn Cys	
165 170 175	
acc ctc ctt gga aag cta gaa gca cac cag ggg aca acg gaa tca gat	576
Thr Leu Leu Gly Lys Leu Glu Ala His Gln Gly Thr Thr Glu Ser Asp	
180 185 190	
gtg gtc tgc agc tct tcc atg aca ctg agg aga cca ccc aag gag gcc	624
Val Val Cys Ser Ser Ser Met Thr Leu Arg Arg Pro Pro Lys Glu Ala	
195 200 205	

cag gct tac ctg ccc agt ctc atc gtt ctg ctc ctc ttc atc tct gtg	672
Gln Ala Tyr Leu Pro Ser Leu Ile Val Leu Leu Leu Phe Ile Ser Val	
210 215 220	
gta gta gtg gct gcc atc atc ttc ggc gtt tac tac agg aag gga ggg	720
Val Val Val Ala Ala Ile Ile Phe Gly Val Tyr Tyr Arg Lys Gly Gly	
225 230 235 240	
aaa gcg ctg aca gct aat ttg tgg aat tgg gtc aat gat gct tgc agt	768
Lys Ala Leu Thr Ala Asn Leu Trp Asn Trp Val Asn Asp Ala Cys Ser	
245 250 255	
agt cta agt gga aat aag gag tcc tca ggg gac cgt tgt gct ggt tcc	816
Ser Leu Ser Gly Asn Lys Glu Ser Ser Gly Asp Arg Cys Ala Gly Ser	
260 265 270	
cac tcg gca acc tcc agt cag caa gaa gtg tgt gaa ggt atc tta cta	864
His Ser Ala Thr Ser Ser Gln Gln Glu Val Cys Glu Gly Ile Leu Leu	
275 280 285	
atg act cgg gag gag aag atg gtt cca gaa gac ggt gct gga gtc tgt	912
Met Thr Arg Glu Glu Lys Met Val Pro Glu Asp Gly Ala Gly Val Cys	
290 295 300	
ggg cct gtg tgt gcg gca ggt ggg ccc tgg gca gaa gtc aga gat tct	960
Gly Pro Val Cys Ala Ala Gly Gly Pro Trp Ala Glu Val Arg Asp Ser	
305 310 315 320	
agg acg ttc aca ctg gtc agc gag gtt gag acg caa gga gac ctc tcg	1008
Arg Thr Phe Thr Leu Val Ser Glu Val Glu Thr Gln Gly Asp Leu Ser	
325 330 335	
agg aag att ccc aca gag gat gag tac acg gac cgg ccc tcg cag cct	1056
Arg Lys Ile Pro Thr Glu Asp Glu Tyr Thr Asp Arg Pro Ser Gln Pro	
340 345 350	
tcg act ggt tca ctg ctc cta atc cag cag gga agc aaa tct ata ccc	1104
Ser Thr Gly Ser Leu Leu Leu Ile Gln Gln Gly Ser Lys Ser Ile Pro	
355 360 365	
cca ttc cag gag ccc ctg gaa gtg ggg gag aac gac agt tta agc cag	1152
Pro Phe Gln Glu Pro Leu Glu Val Gly Glu Asn Asp Ser Leu Ser Gln	
370 375 380	
tgt ttc acc ggg act gaa agc acg gtg gat tct gag ggc tgt gac ttc	1200
Cys Phe Thr Gly Thr Glu Ser Thr Val Asp Ser Glu Gly Cys Asp Phe	
385 390 395 400	
act gag cct ccg agc aga act gac tct atg ccc gtg tcc cct gaa aag	1248
Thr Glu Pro Pro Ser Arg Thr Asp Ser Met Pro Val Ser Pro Glu Lys	
405 410 415	
cac ctg aca aaa gaa ata gaa ggt gac agt tgc ctc ccc tgg gtg gtc	1296
His Leu Thr Lys Glu Ile Glu Gly Asp Ser Cys Leu Pro Trp Val Val	
420 425 430	
agc tcc aac tca aca gat ggc tac aca ggc agt ggg aac act cct ggg	1344
Ser Ser Asn Ser Thr Asp Gly Tyr Thr Gly Ser Gly Asn Thr Pro Gly	
435 440 445	

gag gac cat gaa ccc ttt cca ggg tcc ctg aaa tgt gga cca ttg ccc	1392
Glu Asp His Glu Pro Phe Pro Gly Ser Leu Lys Cys Gly Pro Leu Pro	
450 455 460	
cag tgt gcc tac agc atg ggc ttt ccc agt gaa gca gca gcc agc atg	1440
Gln Cys Ala Tyr Ser Met Gly Phe Pro Ser Glu Ala Ala Ala Ser Met	
465 470 475 480	
gca gag gcg gga gta cgg ccc cag gac agg gct gat gag agg gga gcc	1488
Ala Glu Ala Gly Val Arg Pro Gln Asp Arg Ala Asp Glu Arg Gly Ala	
485 490 495	
tca ggg tcc ggg agc tcc ccc agt gac cag cca cct gcc tct ggg aac	1536
Ser Gly Ser Gly Ser Ser Pro Ser Asp Gln Pro Pro Ala Ser Gly Asn	
500 505 510	
gtg act gga aac agt aac tcc acg ttc atc tct agc ggg cag gtg atg	1584
Val Thr Gly Asn Ser Asn Ser Thr Phe Ile Ser Ser Gly Gln Val Met	
515 520 525	
aac ttc aag ggt gac atc atc gtg gtg tat gtc agc cag acc tcg cag	1632
Asn Phe Lys Gly Asp Ile Ile Val Val Tyr Val Ser Gln Thr Ser Gln	
530 535 540	
gag ggc ccg ggt tcc gca gag ccc gag tcg gag ccc gtg ggc cgc cct	1680
Glu Gly Pro Gly Ser Ala Glu Pro Glu Ser Glu Pro Val Gly Arg Pro	
545 550 555 560	
gtg cag gag gag acg ctg gca cac aga gac tcc ttt gcg ggc acc gcg	1728
Val Gln Glu Glu Thr Leu Ala His Arg Asp Ser Phe Ala Gly Thr Ala	
565 570 575	
ccg cgc ttc ccc gac gtc tgt gcc acc ggg gct ggg ctg cag gag cag	1776
Pro Arg Phe Pro Asp Val Cys Ala Thr Gly Ala Gly Leu Gln Glu Gln	
580 585 590	
ggg gca ccc ccg cag aag gac ggg aca tcg ccg ccg gtg cag gag cag	1824
Gly Ala Pro Arg Gln Lys Asp Gly Thr Ser Arg Pro Val Gln Glu Gln	
595 600 605	
ggt ggg gcg cag act tca ctc cat acc cag ggg tcc gga caa tgt gca	1872
Gly Gly Ala Gln Thr Ser Leu His Thr Gln Gly Ser Gly Gln Cys Ala	
610 615 620	
gaa tga	1878
Glu	
625	

<210> 5
 <211> 625
 <212> PRT
 <213> Murine

<400> 5

Met Ala Pro Arg Ala Arg Arg Arg Arg Gln Leu Pro Ala Pro Leu Leu
1 5 10 15

Ala Leu Cys Val Leu Leu Val Pro Leu Gln Val Thr Leu Gln Val Thr

20

25

30

Pro Pro Cys Thr Gln Glu Arg His Tyr Glu His Leu Gly Arg Cys Cys
 35 40 45

Ser Arg Cys Glu Pro Gly Lys Tyr Leu Ser Ser Lys Cys Thr Pro Thr
 50 55 60

Ser Asp Ser Val Cys Leu Pro Cys Gly Pro Asp Glu Tyr Leu Asp Thr
 65 70 75 80

Trp Asn Glu Glu Asp Lys Cys Leu Leu His Lys Val Cys Asp Ala Gly
 85 90 95

Lys Ala Leu Val Ala Val Asp Pro Gly Asn His Thr Ala Pro Arg Arg
 100 105 110

Cys Ala Cys Thr Ala Gly Tyr His Trp Asn Ser Asp Cys Glu Cys Cys
 115 120 125

Arg Arg Asn Thr Glu Cys Ala Pro Gly Phe Gly Ala Gln His Pro Leu
 130 135 140

Gln Leu Asn Lys Asp Thr Val Cys Thr Pro Cys Leu Leu Gly Phe Phe
 145 150 155 160

Ser Asp Val Phe Ser Ser Thr Asp Lys Cys Lys Pro Trp Thr Asn Cys
 165 170 175

Thr Leu Leu Gly Lys Leu Glu Ala His Gln Gly Thr Thr Glu Ser Asp
 180 185 190

Val Val Cys Ser Ser Ser Met Thr Leu Arg Arg Pro Pro Lys Glu Ala
 195 200 205

Gln Ala Tyr Leu Pro Ser Leu Ile Val Leu Leu Leu Phe Ile Ser Val
 210 215 220

Val Val Val Ala Ala Ile Ile Phe Gly Val Tyr Tyr Arg Lys Gly Gly
 225 230 235 240

Lys Ala Leu Thr Ala Asn Leu Trp Asn Trp Val Asn Asp Ala Cys Ser
 245 250 255

Ser Leu Ser Gly Asn Lys Glu Ser Ser Gly Asp Arg Cys Ala Gly Ser
 260 265 270

His Ser Ala Thr Ser Ser Gln Gln Glu Val Cys Glu Gly Ile Leu Leu
 275 280 285

Met Thr Arg Glu Glu Lys Met Val Pro Glu Asp Gly Ala Gly Val Cys
 290 295 300

Gly Pro Val Cys Ala Ala Gly Gly Pro Trp Ala Glu Val Arg Asp Ser
 305 310 315 320

Arg Thr Phe Thr Leu Val Ser Glu Val Glu Thr Gln Gly Asp Leu Ser
 325 330 335

Arg Lys Ile Pro Thr Glu Asp Glu Tyr Thr Asp Arg Pro Ser Gln Pro
 340 345 350

Ser Thr Gly Ser Leu Leu Leu Ile Gln Gln Gly Ser Lys Ser Ile Pro
 355 360 365

Pro Phe Gln Glu Pro Leu Glu Val Gly Glu Asn Asp Ser Leu Ser Gln
 370 375 380

Cys Phe Thr Gly Thr Glu Ser Thr Val Asp Ser Glu Gly Cys Asp Phe
 385 390 395 400

Thr Glu Pro Pro Ser Arg Thr Asp Ser Met Pro Val Ser Pro Glu Lys
 405 410 415

His Leu Thr Lys Glu Ile Glu Gly Asp Ser Cys Leu Pro Trp Val Val
 420 425 430

Ser Ser Asn Ser Thr Asp Gly Tyr Thr Gly Ser Gly Asn Thr Pro Gly
 435 440 445

Glu Asp His Glu Pro Phe Pro Gly Ser Leu Lys Cys Gly Pro Leu Pro
 450 455 460

Gln Cys Ala Tyr Ser Met Gly Phe Pro Ser Glu Ala Ala Ala Ser Met
 465 470 475 480

Ala Glu Ala Gly Val Arg Pro Gln Asp Arg Ala Asp Glu Arg Gly Ala
 485 490 495

Ser Gly Ser Gly Ser Ser Pro Ser Asp Gln Pro Pro Ala Ser Gly Asn
 500 505 510

Val Thr Gly Asn Ser Asn Ser Thr Phe Ile Ser Ser Gly Gln Val Met
515 520 525

Asn Phe Lys Gly Asp Ile Ile Val Val Tyr Val Ser Gln Thr Ser Gln
530 535 540

Glu Gly Pro Gly Ser Ala Glu Pro Glu Ser Glu Pro Val Gly Arg Pro
545 550 555 560

Val Gln Glu Glu Thr Leu Ala His Arg Asp Ser Phe Ala Gly Thr Ala
565 570 575

Pro Arg Phe Pro Asp Val Cys Ala Thr Gly Ala Gly Leu Gln Glu Gln
580 585 590

Gly Ala Pro Arg Gln Lys Asp Gly Thr Ser Arg Pro Val Gln Glu Gln
595 600 605

Gly Gly Ala Gln Thr Ser Leu His Thr Gln Gly Ser Gly Gln Cys Ala
610 615 620

Glu
625

<210> 6
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<223> Murine

<400> 6

Arg Met Lys Gln Ile Glu Asp Lys Ile Glu Glu Ile Leu Ser Lys Ile
1 5 10 15

Tyr His Ile Glu Asn Glu Ile Ala Arg Ile Lys Lys Leu Ile Gly Glu
20 25 30

Arg

<210> 7
<211> 954
<212> DNA
<213> Homo sapiens;
<220>

<221> CDS
 <222> (1)..(951)
 <223>

<400> 7

atg cgc cgc gcc agc aga gac tac acc aag tac ctg cgt ggc tcg gag	48
Met Arg Arg Ala Ser Arg Asp Tyr Thr Lys Tyr Leu Arg Gly Ser Glu	
1 5 10 15	
gag atg ggc ggc ggc ccc gga gcc ccg cac gag ggc ccc ctg cac gcc	96
Glu Met Gly Gly Gly Pro Gly Ala Pro His Glu Gly Pro Leu His Ala	
20 25 30	
ccg ccg ccg cct gcg ccg cac cag ccc ccc gcc gcc tcc cgc tcc atg	144
Pro Pro Pro Pro Ala Pro His Gln Pro Pro Ala Ala Ser Arg Ser Met	
35 40 45	
ttc gtg gcc ctc ctg ggg ctg ggg ctg ggc cag gtt gtc tgc agc gtc	192
Phe Val Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser Val	
50 55 60	
gcc ctg ttc ttc tat ttc aga gcg cag atg gat cct aat aga ata tca	240
Ala Leu Phe Phe Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile Ser	
65 70 75 80	
gaa gat ggc act cac tgc att tat aga att ttg aga ctc cat gaa aat	288
Glu Asp Gly Thr His Cys Ile Tyr Arg Ile Leu Arg Leu His Glu Asn	
85 90 95	
gca gat ttt caa gac aca act ctg gag agt caa gat aca aaa tta ata	336
Ala Asp Phe Gln Asp Thr Thr Leu Glu Ser Gln Asp Thr Lys Leu Ile	
100 105 110	
cct gat tca tgt agg aga att aaa cag gcc ttt caa gga gct gtg caa	384
Pro Asp Ser Cys Arg Arg Ile Lys Gln Ala Phe Gln Gly Ala Val Gln	
115 120 125	
aag gaa tta caa cat atc gtt gga tca cag cac atc aga gca gag aaa	432
Lys Glu Leu Gln His Ile Val Gly Ser Gln His Ile Arg Ala Glu Lys	
130 135 140	
gcg atg gtg gat ggc tca tgg tta gat ctg gcc aag agg agc aag ctt	480
Ala Met Val Asp Gly Ser Trp Leu Asp Leu Ala Lys Arg Ser Lys Leu	
145 150 155 160	
gaa gct cag cct ttt gct cat ctc act att aat gcc acc gac atc cca	528
Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Thr Asp Ile Pro	
165 170 175	
tct ggt tcc cat aaa gtg agt ctg tcc tct tgg tac cat gat cgg ggt	576
Ser Gly Ser His Lys Val Ser Leu Ser Ser Trp Tyr His Asp Arg Gly	
180 185 190	
tgg gcc aag atc tcc aac atg act ttt agc aat gga aaa cta ata gtt	624
Trp Ala Lys Ile Ser Asn Met Thr Phe Ser Asn Gly Lys Leu Ile Val	
195 200 205	
aat cag gat ggc ttt tat tac ctg tat gcc aac att tgc ttt cga cat	672
Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His	
210 215 220	

cat gaa act tca gga gac cta gct aca gag tat ctt caa cta atg gtg 720
His Glu Thr Ser Gly Asp Leu Ala Thr Glu Tyr Leu Gln Leu Met Val
225 230 235 240

aaa gga gga agc acc aag tat tgg tca ggg aat tct gaa ttc cat ttt 816
Lys Gly Gly Ser Thr Lys Tyr Trp Ser Gly Asn Ser Glu Phe His Phe
260 265 270

atc agc atc gag gtc tcc aac ccc tcc tta ctg gat ccg gat cag gat 912
Ile Ser Ile Glu Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp
290 295 300

```
<210>      8
<211>     317
<212>     PRT
<213>     Homo sapiens;
```


Pro Asp Ser Cys Arg Arg Ile Lys Gln Ala Phe Gln Gly Ala Val Gln
115 120 125

Lys Glu Leu Gln His Ile Val Gly Ser Gln His Ile Arg Ala Glu Lys
130 135 140

Ala Met Val Asp Gly Ser Trp Leu Asp Leu Ala Lys Arg Ser Lys Leu
145 150 155 160

Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Thr Asp Ile Pro
165 170 175

Ser Gly Ser His Lys Val Ser Leu Ser Ser Trp Tyr His Asp Arg Gly
180 185 190

Trp Ala Lys Ile Ser Asn Met Thr Phe Ser Asn Gly Lys Leu Ile Val
195 200 205

Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His
210 215 220

His Glu Thr Ser Gly Asp Leu Ala Thr Glu Tyr Leu Gln Leu Met Val
225 230 235 240

Tyr Val Thr Lys Thr Ser Ile Lys Ile Pro Ser Ser His Thr Leu Met
245 250 255

Lys Gly Gly Ser Thr Lys Tyr Trp Ser Gly Asn Ser Glu Phe His Phe
260 265 270

Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ser Gly Glu Glu
275 280 285

Ile Ser Ile Glu Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp
290 295 300

Ala Thr Tyr Phe Gly Ala Phe Lys Val Arg Asp Ile Asp
305 310 315